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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/780,532

DATE: 03/08/2001
TIME: 11:41:54

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03082001\I780532.raw

3 <110> APPLICANT: Wood, Clive
4 Chaudhary, Divya
5 Long, Andrew
7 <120> TITLE OF INVENTION: TRADE MOLECULES, AND USES RELATED THERETO
9 <130> FILE REFERENCE: GNN-012CP
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/780,532
C--> 12 <141> CURRENT FILING DATE: 2001-02-09
14 <150> PRIOR APPLICATION NUMBER: 60/181,922
15 <151> PRIOR FILING DATE: 2000-02-11
17 <150> PRIOR APPLICATION NUMBER: 60/182,148
18 <151> PRIOR FILING DATE: 2000-02-14
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1660
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1251)
33 <400> SEQUENCE: 1
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35 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
36 1 5 10 15
38 tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa tca gga 96
39 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
40 20 25 30
42 gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac ttt tgt ccc 144
43 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
44 35 40 45
46 tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc 192
47 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
48 50 55 60
50 ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc 240
51 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
52 65 70 75 80
54 aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca 288
55 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
56 85 90 95
58 gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc 336
59 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
60 100 105 110
62 atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc 384
63 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
64 115 120 125
66 ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct cct 432
67 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro

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68	130	135	140	
70	tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc			480
71	Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser			
72	145	150	155	160
74	acg gcc tcc agc cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc			528
75	Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Val Ile Cys Ser			
76	165	170	175	
78	gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat			576
79	Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr			
80	180	185	190	
82	tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca			624
83	Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser			
84	195	200	205	
86	cag gac att cag tac aac ggc tct gag ctg tcg tgt ttt gac aga cct			672
87	Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro			
88	210	215	220	
90	cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac			720
91	Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp			
92	225	230	235	240
94	tca gtg cag acc tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt			768
95	Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys			
96	245	250	255	
98	gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat			816
99	Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His			
100	260	265	270	
102	tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg			864
103	Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met			
104	275	280	285	
106	gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt			912
107	Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe			
108	290	295	300	
110	tca gat gcc tgg cct ctg atg cag aat ccc atg ggt gac aac atc			960
111	Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile			
112	305	310	315	320
114	tct ttt tgt gac tct tat cct gaa ctc act gga gaa gac att cat tct			1008
115	Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser			
116	325	330	335	
118	ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt			1056
119	Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser			
120	340	345	350	
122	caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac			1104
123	Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn			
124	355	360	365	
126	ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa			1152
127	Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu			
128	370	375	380	
130	tca gca tca act cag gat gca cta act atg aga agc cag cta gat gag			1200
131	Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln			
132	385	390	395	400

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134 gag agt ggc gct atc atc cac cca gcc act cag acg tcc ctc cag gaa 1248
 135 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
 136 405 410 415
 138 gct' taaagaacct gcttcttct gcagtagaaag cgtgtgctgg aacccaaaga 1301
 139 Ala
 141 gtactcctt gtaggccta tggactgagc agtctggacc ttgcatggct tctggggcaa 1361
 143 aaatgaatct gaaccaaact gacgcattt gaagcctttc agccagtgc ttctgagcca 1421
 145 gaccagctgt aagctgaac ctcaatgaat aacaagaaaa gactccaggc cgactcatga 1481
 147 tactctgcat tttcctaca tgagaagctt ctctgccaca aaagtgactt caaagacgga 1541
 149 tgggttgagc tggcagccta tgagattgtg gacatataac aagaaacaga aatgccctca 1601
 151 tgcttatttt catggtgat gtgggtttac aagactgaag acccagagta tacttttc 1660
 154 <210> SEQ ID NO: 2
 155 <211> LENGTH: 417
 156 <212> TYPE: PRT
 157 <213> ORGANISM: Homo sapiens
 159 <400> SEQUENCE: 2
 160 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
 161 1 5 10 15
 163 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
 164 20 25 30
 166 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 167 35 40 45
 169 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 170 50 55 60
 172 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
 173 65 70 75 80
 175 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
 176 85 90 95
 178 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
 179 100 105 110
 181 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 182 115 120 125
 184 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 185 130 135 140
 187 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
 188 145 150 155 160
 190 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 191 165 170 175
 193 Ala Leu Ala Thr Val Leu Leu Ala Leu Ile Leu Cys Val Ile Tyr
 194 180 185 190
 196 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
 197 195 200 205
 199 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro
 200 210 215 220
 202 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
 203 225 230 235 240
 205 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
 206 245 250 255
 208 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His

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209	260	265	270
211 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met			
212 275	280	285	
214 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe			
215 290	295	300	
217 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile			
218 305	310	315	320
220 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser			
221 325	330	335	
223 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser			
224 340	345	350	
226 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn			
227 355	360	365	
229 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu			
230 370	375	380	
232 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln			
233 385	390	395	400
235 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu			
236 405	410	415	
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243 <211> LENGTH: 1325			
244 <212> TYPE: DNA			
245 <213> ORGANISM: Homo sapiens			
247 <220> FEATURE:			
248 <221> NAME/KEY: CDS			
249 <222> LOCATION: (1)...(1269)			
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254 1 5 10 15			
256 tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga	96		
257 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly			
258 20 25 30			
260 gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc	144		
261 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro			
262 35 40 45			
264 tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc	192		
265 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe			
266 50 55 60			
268 ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc	240		
269 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe			
270 65 70 75 80			
272 aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca	288		
273 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala			
274 85 90 95			
276 gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc	336		
277 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala			
278 100 105 110			

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280 atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc	384
281 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
282 115 120 125	
284 ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct	432
285 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro	
286 130 135 140	
288 tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc	480
289 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser	
290 145 150 155 160	
292 acg gcc tcc agc cca ccg gac acg gcg ctg gct gcc gtt atc tgc agc	528
293 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Val Ile Cys Ser	
294 165 170 175	
296 gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat	576
297 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr	
298 180 185 190	
300 tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca	624
301 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser	
302 195 200 205	
304 cag gac att cag tac aac ggc tct gag ctg tgc tgt ctt gac aga cct	672
305 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro	
306 210 215 220	
308 cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac	720
309 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp	
310 225 230 235 240	
312 tca gtg cag acc tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt	768
313 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys	
314 245 250 255	
316 gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat	816
317 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His	
318 260 265 270	
320 tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg	864
321 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met	
322 275 280 285	
324 gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt	912
325 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe	
326 290 295 300	
328 tca gat gcc tgg cct ctg atg cag aat ccc atg ggt ggt gac aac atc	960
329 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile	
330 305 310 315 320	
332 tct ttt tgt gac tct tat cct gaa ctc gct gga gaa gac att cat tct	1008
333 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Ala Gly Glu Asp Ile His Ser	
334 325 330 335	
336 ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt	1056
337 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser	
338 340 345 350	
340 caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac	1104
341 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn	
342 355 360 365	
344 ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa	1152

VERIFICATION SUMMARY
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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date